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The genome-wide structure of the Jewish people

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Abstract

Contemporary Jews comprise an aggregate of ethno-religious communities whose worldwide members identify with each other through various shared religious, historical and cultural traditions^{1,2}. Historical evidence suggests common origins in the Middle East, followed by migrations leading to the establishment of communities of Jews in Europe, Africa and Asia, in what is termed the Jewish Diaspora^{3,4,5}. This complex demographic history imposes special challenges in attempting to address the genetic structure of the Jewish people⁶. Although many genetic studies have shed light on Jewish origins and on diseases prevalent among Jewish communities, including studies focusing on uniparentally and biparentally inherited markers^{7,8,9,10,11,12,13,14,15,16}, genome-wide patterns of variation across the vast geographic span of Jewish Diaspora communities and their respective neighbours have yet to be addressed. Here we use high-density bead arrays to genotype individuals from 14 Jewish Diaspora communities and compare these patterns of genome-wide diversity with those from 69 Old World non-Jewish populations, of which 25 have not previously been reported. These samples were carefully chosen to provide comprehensive comparisons between Jewish and non-Jewish populations in the Diaspora, as well as with non-Jewish populations from the Middle East and north Africa. Principal component and structure-like analyses identify previously unrecognized genetic substructure within the Middle East. Most Jewish samples form a remarkably tight subcluster that overlies Druze and Cypriot samples but not samples from other Levantine populations or paired Diaspora host populations. In contrast, Ethiopian Jews (Beta Israel) and Indian Jews (Bene Israel and Cochini) cluster with neighbouring autochthonous populations in Ethiopia and western India, respectively, despite a clear paternal link between the Bene Israel and the Levant. These results cast light on the variegated genetic architecture of the Middle East, and trace the origins of most Jewish Diaspora communities to the Levant.

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Figure 1: PCA of high-density array data.

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Figure 2: PCA of west Eurasian high-density array data.

Figure 3: Population structure inferred by ADMIXTURE analysis.

Accession codes

Primary accessions Gene Expression Omnibus

- [GSE21478](#)

Data deposits

The array data described in this paper are deposited in the Gene Expression Omnibus under accession number [GSE21478](#).

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Contributions

D.M.B. and R.V. conceived and designed the study. B.B.T., D.C., D.G., D.M.B., E.K.K., G.C., I.K., L.P., M.F.H., O.B., O.S., T.P. and R.V. provided DNA samples to this study. E.M., J.P. and G.Y. screened and prepared the samples for the autosomal genotyping. D.M.B., E.M., G.C., M.F.H. and Si.R. generated and summarized the database for the uniparental analysis. B.Y., M.M. and Sa.R. designed and applied the modelling methodology and statistical analysis. T.P. provided expert input regarding the relevant historical aspects. B.Y., D.M.B., K.S., M.F.H., M.M., R.V. and Sa.R. wrote the paper. B.Y., D.M.B. and M.M. contributed equally to the paper. All authors discussed the results and commented on the manuscript.

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Ethics declarations

Competing interests

The authors declare no competing financial interests.

Supplementary information

Supplementary Information

This file contains Supplementary Notes 1-6, References and Supplementary Tables 1-5. (PDF 1143 kb)

Supplementary Figures

This file contains Supplementary Figures 1 and 3-6 and legends for Supplementary Figures 1-6 (see separate file for Supplementary Figure 2) (PDF 6701 kb)

Supplementary Figure 2

This file shows the Principal Component Analysis of the Old World High-Density Array Data. a, Scatter plot of Old World individuals, showing the first two principal components. Here, the first PC (4.2% of variation, vertical axis) captures primarily differences between sub-Saharan Africans and the rest of the Old World. The second PC (3.4% of variation, horizontal axis) differentiates West Eurasians from South and East Asians. Axes of variation were scaled according to eigenvalues. Each letter code (Supplementary Table 1) corresponds to one individual and the colour indicates population origin. b, Scatter plot of Old World individuals, showing PC1 and PC3. c, Scatter plot of Old World individuals, showing PC1 and PC4. Note that eigenvalues for PC3 and PC4 are ~8 times smaller than for PC1 and 2. (PDF 1892 kb)

PowerPoint slides

PowerPoint slide for Fig. 1

PowerPoint slide for Fig. 2

PowerPoint slide for Fig. 3

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